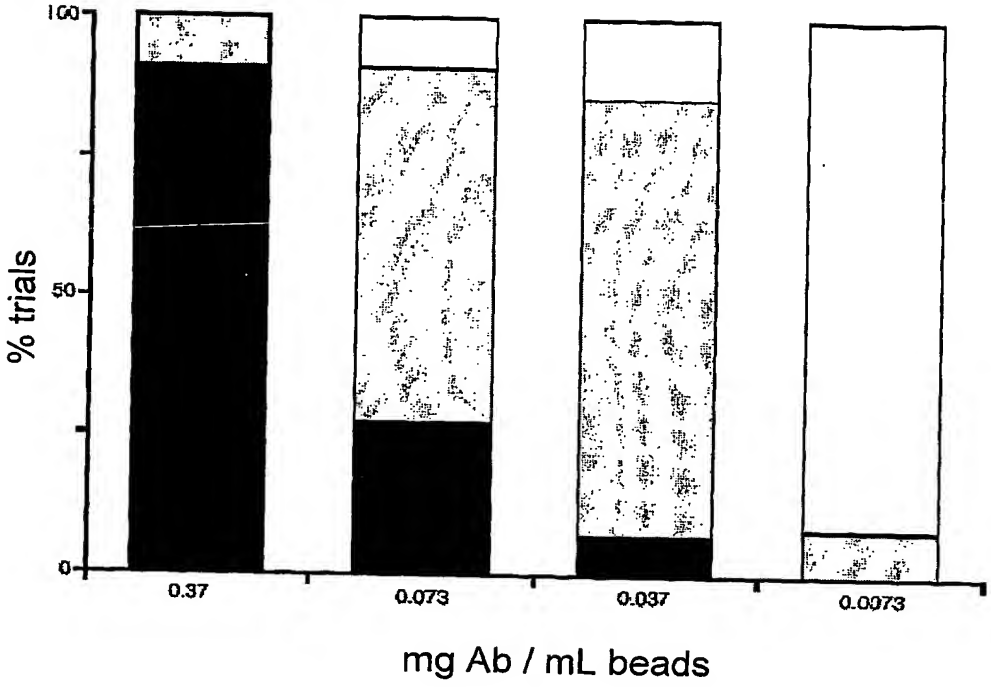

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FIGURE 1

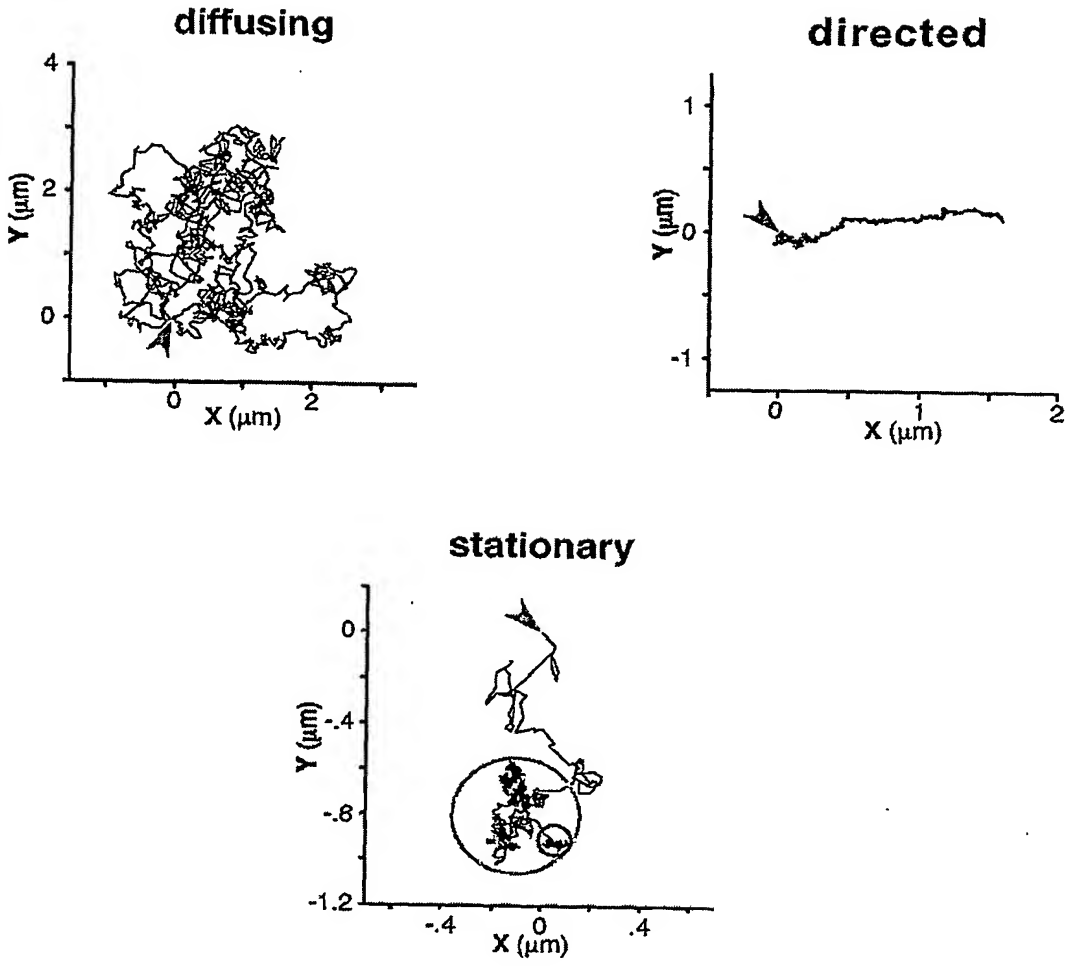

diffusing
4
2
0
Y (μm)
0
2
X (μm)
directed
1
0
-1
Y (μm)
0
1
2
X (μm)
stationary
0
-.4
-.6
-1.2
Y (μm)
-.4
0
.4
X (μm)

FIGURE 2A

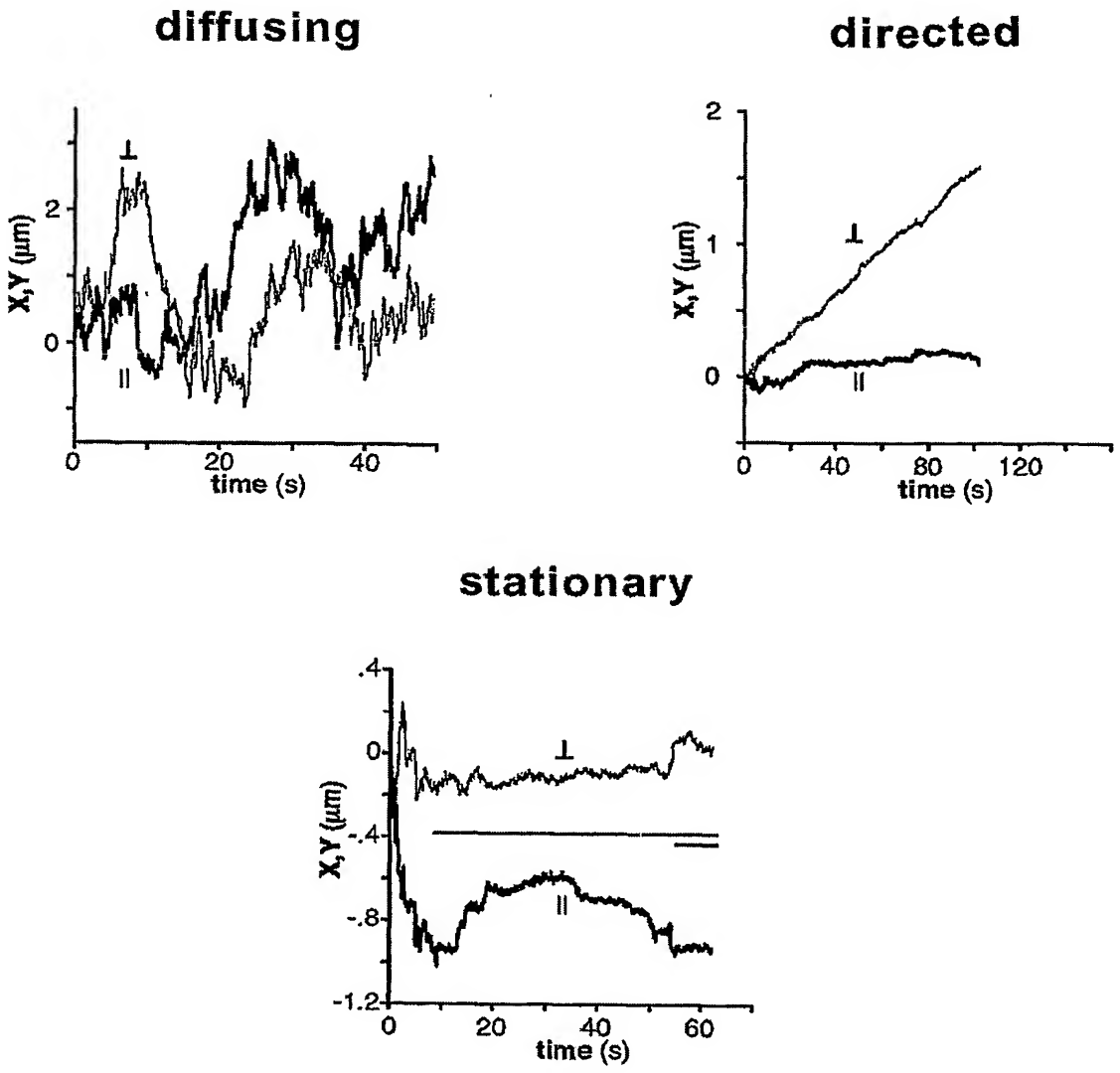


FIGURE 2B

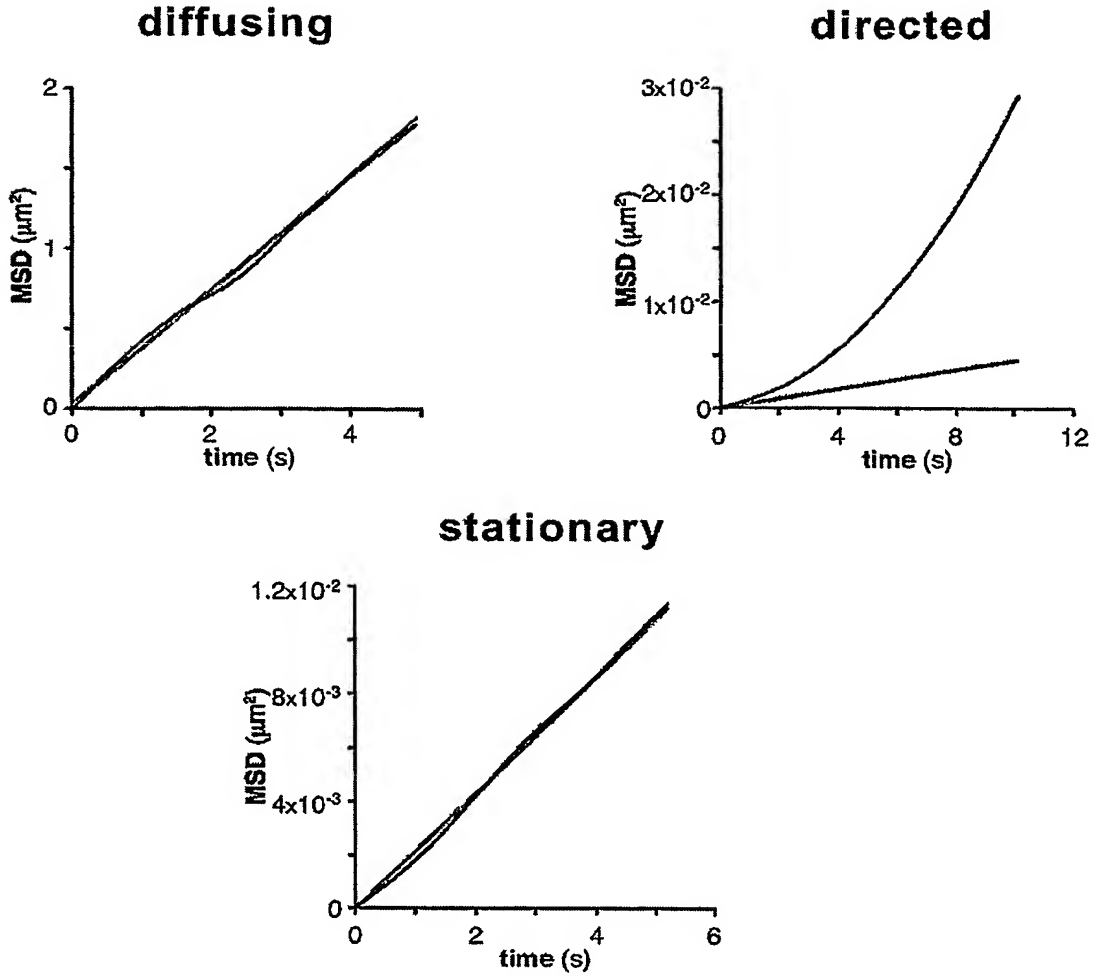
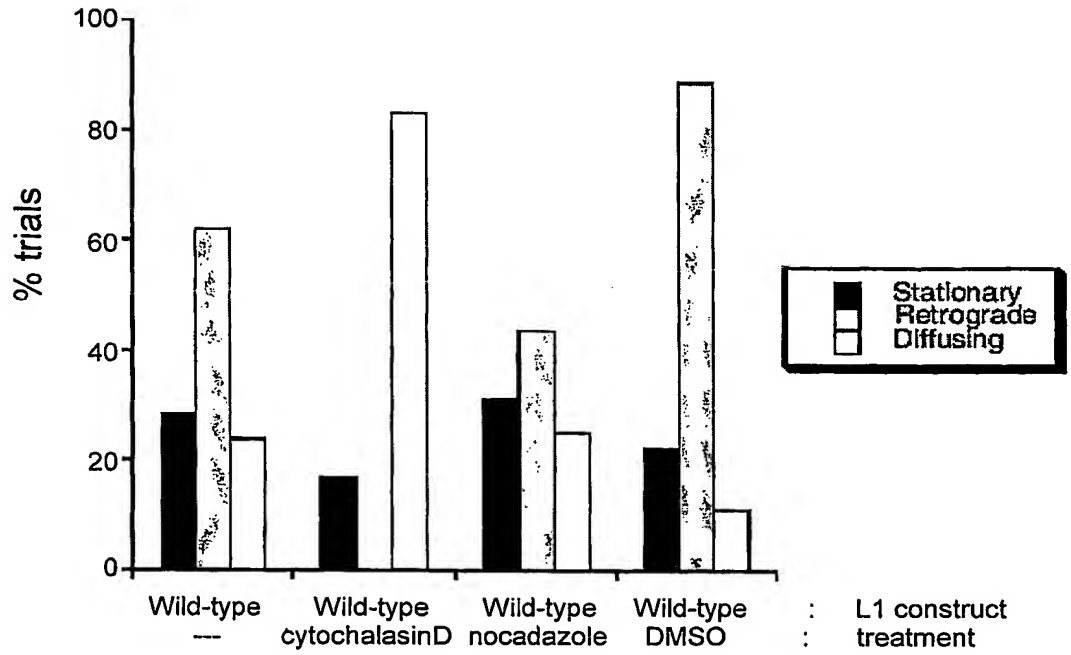

diffusing
MSD (μm²)
time (s)
directed
MSD (μm²)
time (s)
stationary
MSD (μm²)
time (s)

FIGURE 2C


100
80
60
40
20
0
% trials
Stationary
Retrograde
Diffusing
Wild-type

Wild-type
cytochalasinD
Wild-type
nocadazole
Wild-type
DMSO
: L1 construct
: treatment

FIGURE 3A

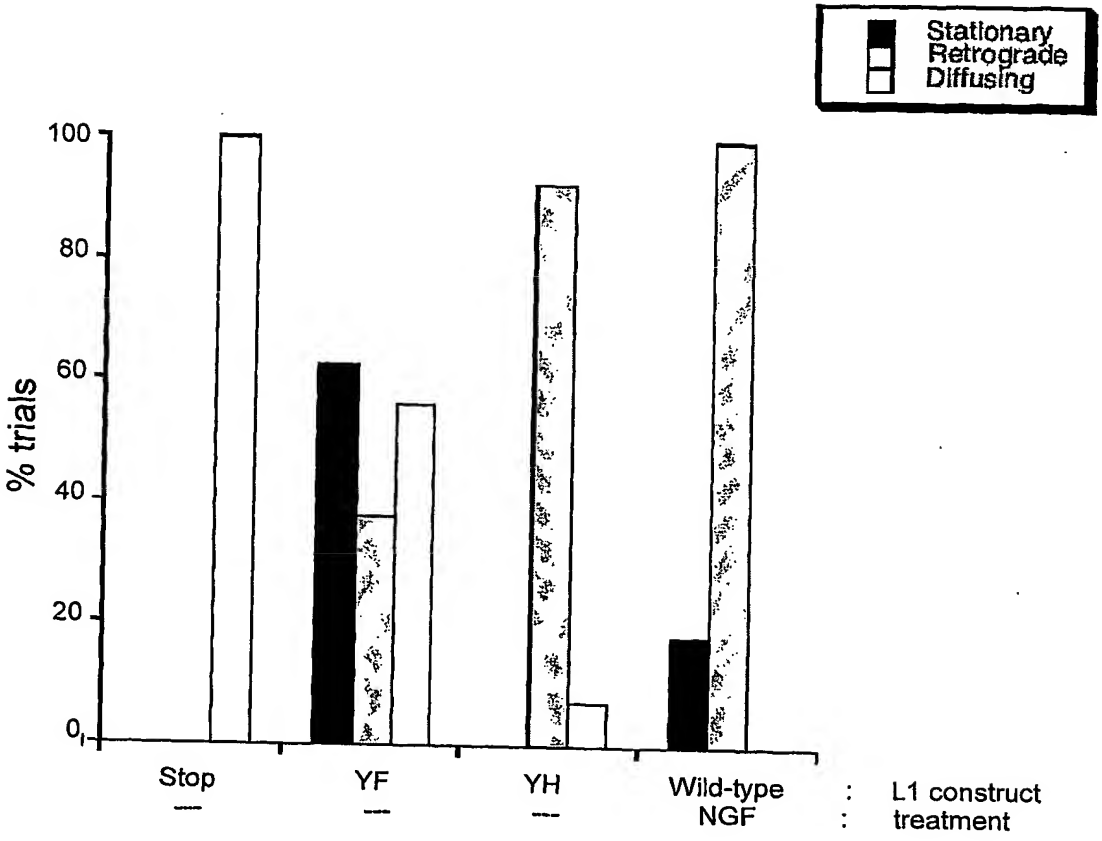

Stationary
Retrograde
Diffusing
100
80
60
40
20
0
% trials
Stop
YF
YH
Wild-type
NGF
: L1 construct
: treatment

FIGURE 3B

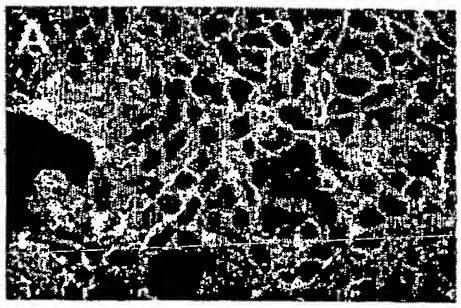


FIGURE 4A

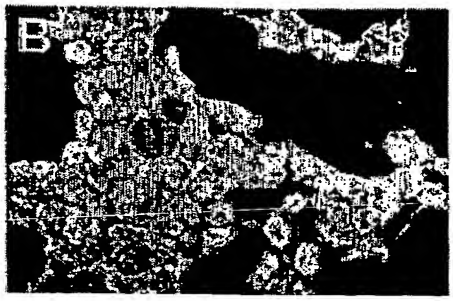


FIGURE 4B

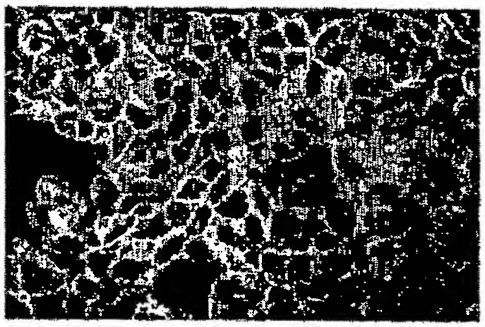


FIGURE 4C

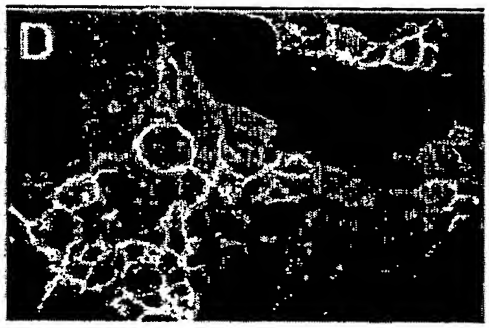


FIGURE 4D

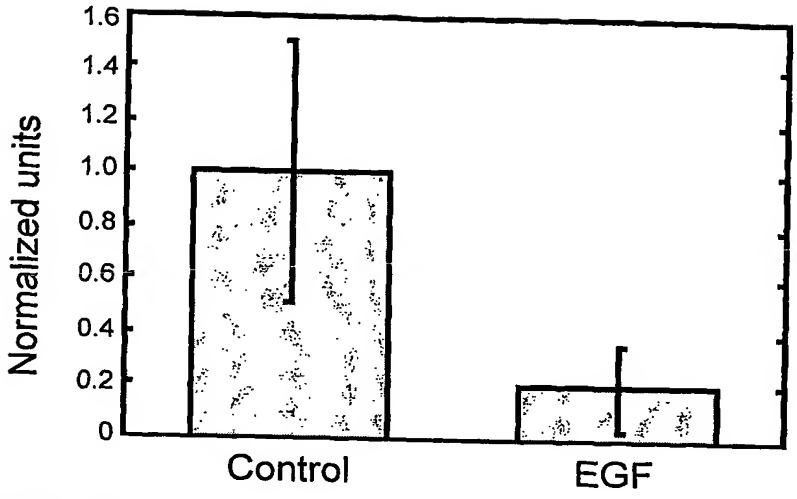


FIGURE 4E

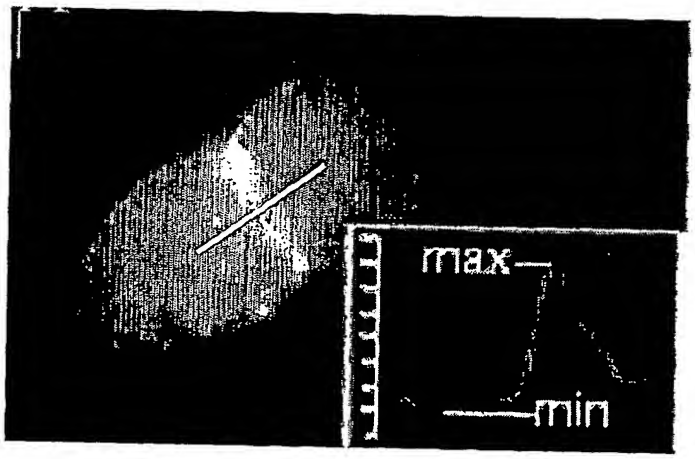


FIGURE 4F

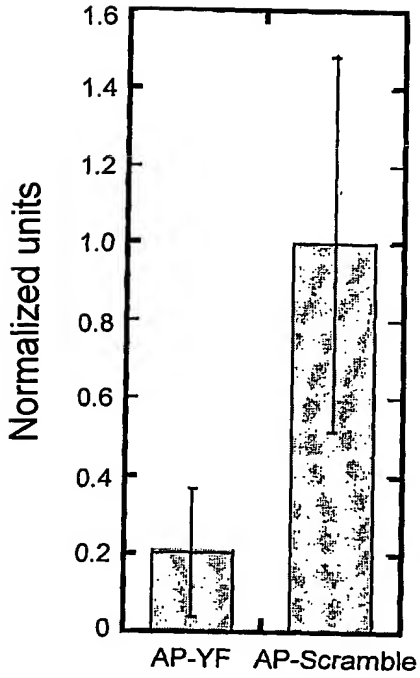


FIGURE 5A

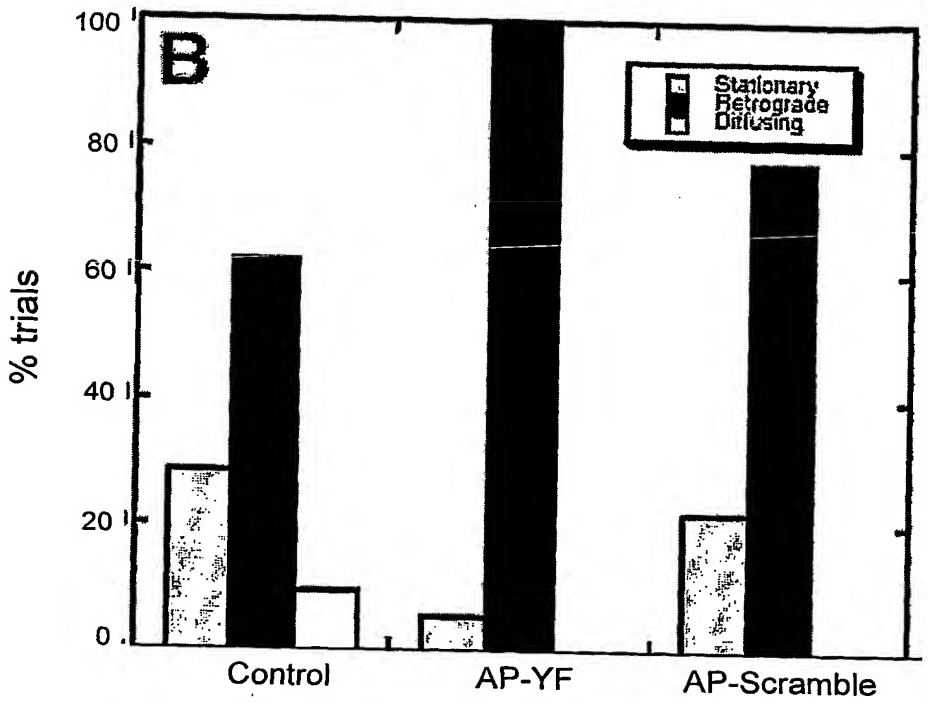
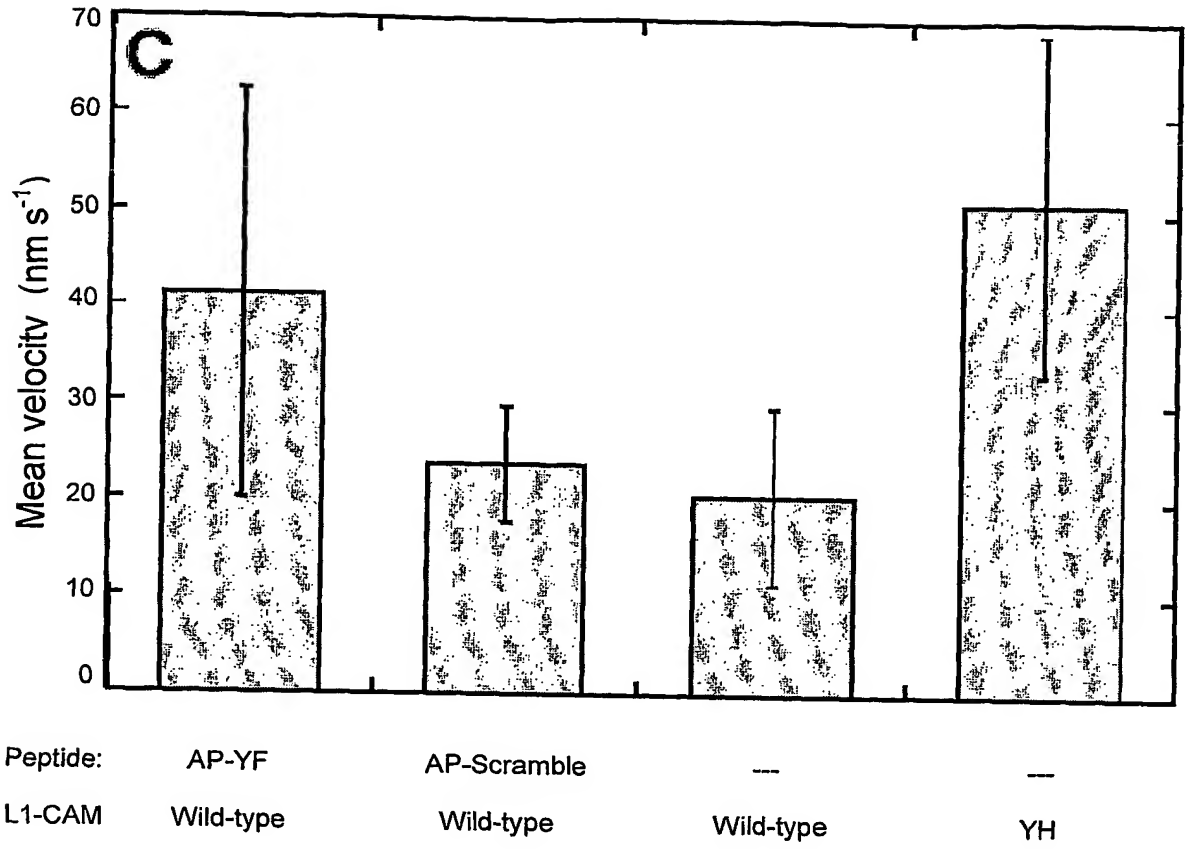

B
Stationary
Retrograde
Diffusing
% trials
100
80
60
40
20
0
Control
AP-YF
AP-Scramble

FIGURE 5B


C
Mean velocity (nm s-1)
70
60
50
40
30
20
10
0
Peptide:
AP-YF
AP-Scramble

L1-CAM
Wild-type
Wild-type
Wild-type
YH

FIGURE 5C

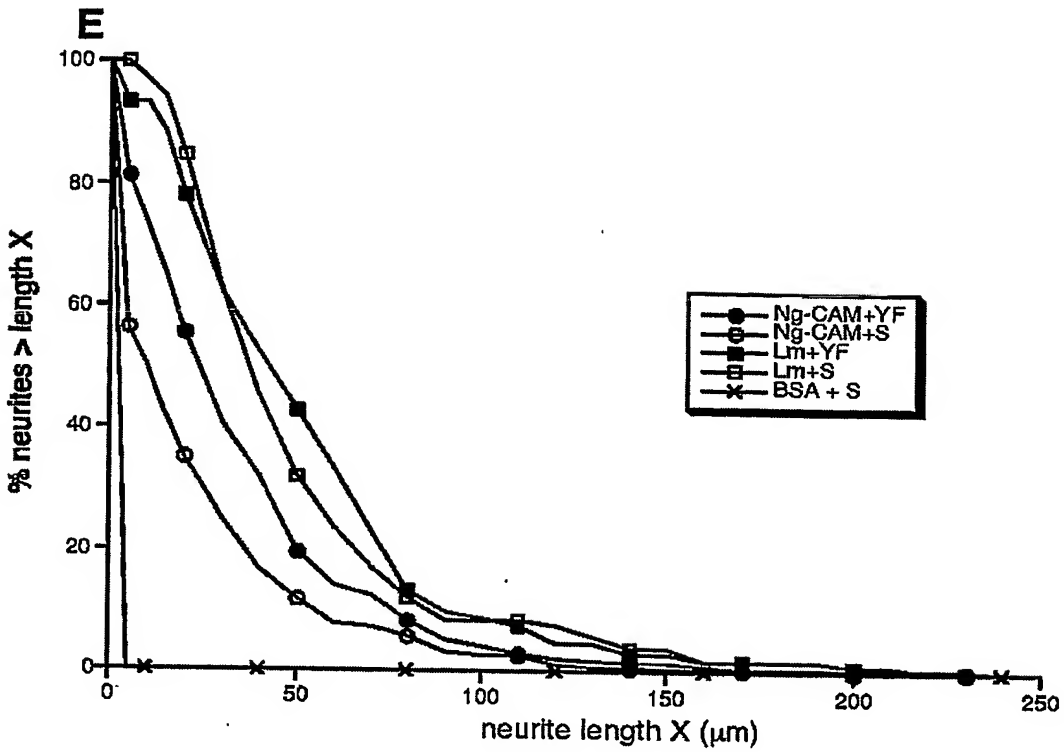

E
100
80
60
40
20
0
% neurites > length X
0
50
100
150
200
250
neurite length X (μm)
Ng-CAM+YF
Ng-CAM+S
Lm+YF
Lm+S
BSA + S

FIGURE 6

```
1     GCTAGCTATG GTCGTGATGC TGCGGTACGT GTGGCCTCTC CTCCTCTGCA GCCCCTGCCT
61    GCTCATACAG ATTCCTGATG AATATAAAGG ACACCATGTA CTAGAGCCAC CTGTCATCAC
121   GGAACAGTCT CCACGGCGCC TGGTTGTCTT CCCAACAGAT GACATAAGCC TCAAATGTGA
181   AGCCAGAGGC AGACCCCAAG TGGAGTTCCG CTGGACGAAA GATGGCATCC ACTTCAAACC
241   TAAGGAAGAA TTGGGTGTAG TGGTACACGA GGCACCCTAT TCTGGCTCCT TCACCATCGA
301   AGGCAACAAC AGCTTTGCCC AGAGGTTTCA GGGCATCTAT CGCTGCTATG CCAGCAATAA
361   TCTAGGAACT GCCATGTCGC ATGAGATCCA GCTCGTGGCT GAGGGTGCCC CCAAATGGCC
421   GAAGGAGACT GTAAAACCCG TGGAAGTGGA GGAAGGAGAA TCAGTAGTTC TACCTTGCAA
481   TCCTCCACCC AGTGCAGCCC CACTTAGGAT CTACTGGATG AACAGCAAGA TTTTGCACAT
541   CAAACAAGAT GAGCGGGTGT CCATGGGCCA GAATGGAGAC CTATATTTTG CCAATGTGCT
601   TACCTCAGAC AATCATTCAG ACTACATCTG CAATGCCCAC TTCCCTGGCA CCCGGACCAT
661   CATTCAAAAG GAACCTATTG ACCTCCGGGT CAAGCCCACC AACAGCATGA TTGACCGGAA
721   GCCACGCCTG CTCTTCCCCA CAAACTCCAG CAGTCACCTC GTGGCCTTGC AGGGCCAGTC
781   ATTAATCCTG GAGTGCATTG CTGAGGGATT CCCTACACCC ACCATCAAGT GGCTGCACCC
841   CAGTGACCCT ATGCCAACAG ACCGTGTTAT CTACCAGAAC CATAACAAGA CACTGCAGCT
901   CCTCAATGTG GGCGAGGAAG ATGATGGCGA GTATACCTGC CTTGCTGAGA ACTCACTGGG
961   CAGTGCTCGG CATGCCTACT ATGTCACTGT GGAAGCTGCC CCATACTGGC TGCAGAAGCC
1021  CCAGAGTCAT TTGTATGGGC CAGGAGAGAC TGCCCGCCTA GACTGCCAAG TCCAGGGCAG
1081  GCCCCAACCA GAGGTCACTT GGAGAATCAA CGGAATGTCT ATAGAGAAGG TGAACAAGGA
1141  CCAGAAGTAC CGGATTGAGC AGGGGTCTTT GATCCTGAGT AATGTGCAAC CAAGTGACAC
1201  AATGGTGACC CAGTGTGAAG CTCGCAACCA GCATGGGCTC CTACTAGCCA ATGCCTATAT
1261  CTATGTTGTC CAGCTGCCAG CCAGGATCCT AACAAAAGAC AATCAGACAT ACATGGCAGT
1321  AGAGGGCAGT ACTGCTTACT TGCTGTGCAA AGCCTTTGGA GCTCCTGTTC CCAGTGTCCA
1381  GTGGCTGGAT GAGGAAGGAA CCACAGTGCT TCAGGATGAA AGATTTTTCC CCTATGCCAA
1441  TGGAACGCTG GGCATCAGAG ATCTCCAGGC CAATGACACT GGACGCTATT TCTGCCAGGC
1501  TGCCAATGAC CAGAACAATG TGACCATTTT GGCTAACCTA CAGGTTAAAG AAGCAACCCA
1561  GATCACACAA GGACCCCGGA GCACAATTGA GAAGAAAGGT GCAAGGGTGA CATTCACGTG
1621  CCAGGCCTCC TTTGACCCCT CTTTACAAGC CAGCATCACT TGGCGTGGAG ATGGGAGAGA
1681  CCTCCAGGAA CGTGGAGACA GTGACAAGTA TTTCATAGAA GATGGGCAAC TTGTCATCCA
1741  GAGCCTGGAC TACAGTGACC AGGGCAACTA CAGTTGTGTG GCCAGCACTG AACTGGATGA
1801  GGTGGAGAGC AGGGCACAAC TCTTAGTGGT GGGAAGCCCT GGGCCAGTGC CTCACCTGGA
1861  GCTGTCCGAC CGCCACTTGC TGAAGCAGAG CCAGGTGCAC TTGTCTTGGA GCCCTGCTGA
1921  AGACCACAAC TCTCCCATTG AGAAATATGA CATTGAATTT GAGGACAAGG AAATGGCTCC
1981  TGAGAAATGG TTCAGTCTAG GCAAGGTGCC AGGAAATCAG ACCTCTACTA CCCTCAAGCT
2041  GTCCCCCTAT GTCCACTATA CCTTTCGGGT CACTGCCATT AACAAATATG GTCCCGGAGA
2101  ACCCAGCCCT GTCTCTGAGA CTGTAGTCAC ACCTGAGGCA GCCCCAGAGA AGAACCCTGT
2161  GGATGTGAGA GGGGAAGGAA ATGAGACCAA CAATATGGTC ATCACATGGA AGCCCCTTCG
2221  GTGGATGGAT TGGAATGCCC CCCAGATTCA GTACCGTGTA CAGTGGCGAC CACTGGGCAA
2281  ACAAGAGACC TGGAAGGAAC AGACCGTGAG CGACCCCTTC CTGGTGGTGT CTAACACTTC
2341  CACATTTGTG CCTTATGAGA TCAAAGTCCA GGCAGTGAAC AACCAGGGGA AGGGCCCTGA
2401  GCCCCAGGTC ACCATTGGCT ATTCAGGGGA AGACTACCCC CAGGTGAGCC CTGAGCTTGA
2461  AGACATCACA ATCTTCAACT CAAGCACTGT GCTGGTCAGG TGGAGGCCTG TGGACTTGGC
2521  CCAGGTTAAG GGCCACCTCA GGGGATACAA TGTAACGTAC TGGTGGAAGG GCAGTCAGAG
2581  AAAGCACAGC AAGAGGCATG TCCACAAAAG TCACATGGTG GTACCTGCGA ACACCACCAG
2641  TGCCATCCTC AGTGGTTTGC GTCCTTACAG CTCTTATCAT GTGGAGGTAC AGGCCTTTAA
2701  TGGGCGGGGC TTAGGGCCTG CAAGTGAATG GACCTTCAGC ACCCCAGAGG GAGTGCCTGG
```

FIGURE 7A

```
2761 CCACCCTGAG GCATTACATC TGGAGTGCCA GTCGGACACT AGCCTGCTAC TGCACTGGCA
2821 GCCACCACTC AGCCACAATG GAGTGCTCAC TGGCTACCTG CTCTCTTACC ATCCCTTGGA
2881 TGGGGAAAGC AAAGAGCAGT TGTTCTTCAA CCTTTCGGAC CCAGAGCTCC GGACTCATAA
2941 TCTCACCAAC CTCAACCCTG ATCTACAGTA CCGCTTCCAG CTTCAGGCCA CCACCCAACA
3001 GGGTCCTGGT GAGGCCATTG TGCGTGAAGG AGGCACTATG GCCCTATTTG GCAAGCCAGA
3061 TTTTGGCAAC ATTTCAGTCA CAGCAGGTGA AAACTACAGT GTGGTCTCCT GGGTCCCTCG
3121 GGAGGGCCAG TGCAATTTCA GGTTCCACAT CCTGTTCAAA GCCTTGCCAG AAGGGAAAGT
3181 GAGCCCTGAT CACCAGCCTC AGCCTCAATA TGTGAGCTAC AATCAGAGCT CCTACACACA
3241 GTGGGACCTA CAGCCTGACA CCAAATATGA GATCCACCTG ATGAGGGAGA AGGTCCTCTT
3301 GCACCATCTG GCTGTGAAGA CTAATGGCAC TGGCCCCGTG CGAGTGTCGA CTACCGGTAG
3361 CTTTGCCTCC GAGGGCTGGT TCATCGCCTT TGTCAGTGCT ATCATTCTCT TGCTCCTCAT
3421 CCTGCTCATC CTCTGCTTCA TCAAACGCAG CAAGGGCGGC AAATATTCAG TGAAGGACAA
3481 GGAGGACACT CAGGTAGATT CCGAGGCCCG GCCCATGAAA GACGAGACCT TCGGCGAGTA
3541 CAGGTCCCTG GAGAGTGACA ATGAAGAGAA GGCCTTCGGC AGCAGCCAGC CATCTCTCAA
3601 TGGAGACATC AAACCCCTAG GCAGTGATGA CAGTCTGGCT GATTATGGGG GCAGTGTGGA
3661 TGTCCAGTTC AATGAGGATG GCTCTTTCAT CGGCCAATAC AGTGGCAAAA AAGAGAAGGA
3721 GGCAGCGGGA GGCAATGACA GCTCAGGGGC TACCTCTCCT ATCAATCCTG CAGTAGCCCT
3781 AGAA***TAG***CAA G<u>CTCGAG</u>
```

FIGURE 7B

```
1    MVVMLRYVWP LLLCSPCLLI QIPDEYKGHH VLEPPVITEQ SPRRLVVFPT
51   DDISLKCEAR GRPQVEFRWT KDGIHFKPKE ELGVVVHEAP YSGSFTIEGN
101  NSFAQRFQGI YRCYASNNLG TAMSHEIQLV AEGAPKWPKE TVKPVEVEEG
151  ESVVLPCNPP PSAAPLRIYW MNSKILHIKQ DERVSMGQNG DLYFANVLTS
201  DNHSDYICNA HFPGTRTIIQ KEPIDLRVKP TNSMIDRKPR LLFPTNSSSH
251  LVALQGQSLI LECIAEGFPT PTIKWLHPSD PMPTDRVIYQ NHNKTLQLLN
301  VGEEDDGEYT CLAENSLGSA RHAYYVTVEA APYWLQKPQS HLYGPGETAR
351  LDCQVQGRPQ PEVTWRINGM SIEKVNKDQK YRIEQGSLIL SNVQPSDTMV
401  TQCEARNQHG LLLANAYIYV VQLPARILTK DNQTYMAVEG STAYLLCKAF
451  GAPVPSVQWL DEEGTTVLQD ERFFPYANGT LGIRDLQAND TGRYFCQAAN
501  DQNNVTILAN LQVKEATQIT QGPRSTIEKK GARVTFTCQA SFDPSLQASI
551  TWRGDGRDLQ ERGDSDKYFI EDGQLVIQSL DYSDQGNYSC VASTELDEVE
601  SRAQLLVVGS PGPVPHLELS DRHLLKQSQV HLSWSPAEDH NSPIEKYDIE
651  FEDKEMAPEK WFSLGKVPGN QTSTTLKLSP YVHYTFRVTA INKYGPGEPS
701  PVSETVVTPE AAPEKNPVDV RGEGNETNNM VITWKPLRWM DWNAPQIQYR
751  VQWRPLGKQE TWKEQTVSDP FLVVSNTSTF VPYEIKVQAV NNQGKGPEPQ
801  VTIGYSGEDY PQVSPELEDI TIFNSSTVLV RWRPVDLAQV KGHLRGYNVT
851  YWWKGSQRKH SKRHVHKSHM VVPANTTSAI LSGLRPYSSY HVEVQAFNGR
901  GLGPASEWTF STPEGVPGHP EALHLECQSD TSLLLHWQPP LSHNGVLTGY
951  LLSYHPLDGE SKEQLFFNLS DPELRTHNLT NLNPDLQYRF QLQATTQQGP
```

FIGURE 8A

1001 GEAIVREGGT MALFGKPDFG NISVTAGENY SVVSWVPREG QCNFRFHILF

1051 KALPEGKVSP DHQPQPQYVS YNQSSYTQWD LQPDTKYEIH LMREKVLLHH

1101 LAVKTNGTGP VRVSTTGSFA SEGWFIAFVS AIILLLLLIL ILCFIKRSKG

1151 GKYSVKDKED TQVDSEARPM KDETFGEY**RS LE**SDNEEKAF GSSQPSLNGD

1201 IKPLGSDDSL ADYGGSVDVQ FNEDGSFIGQ YSGKKEKEAA GGNDSSGATS

1251 PINPAVALE

FIGURE 8B

Figure 9

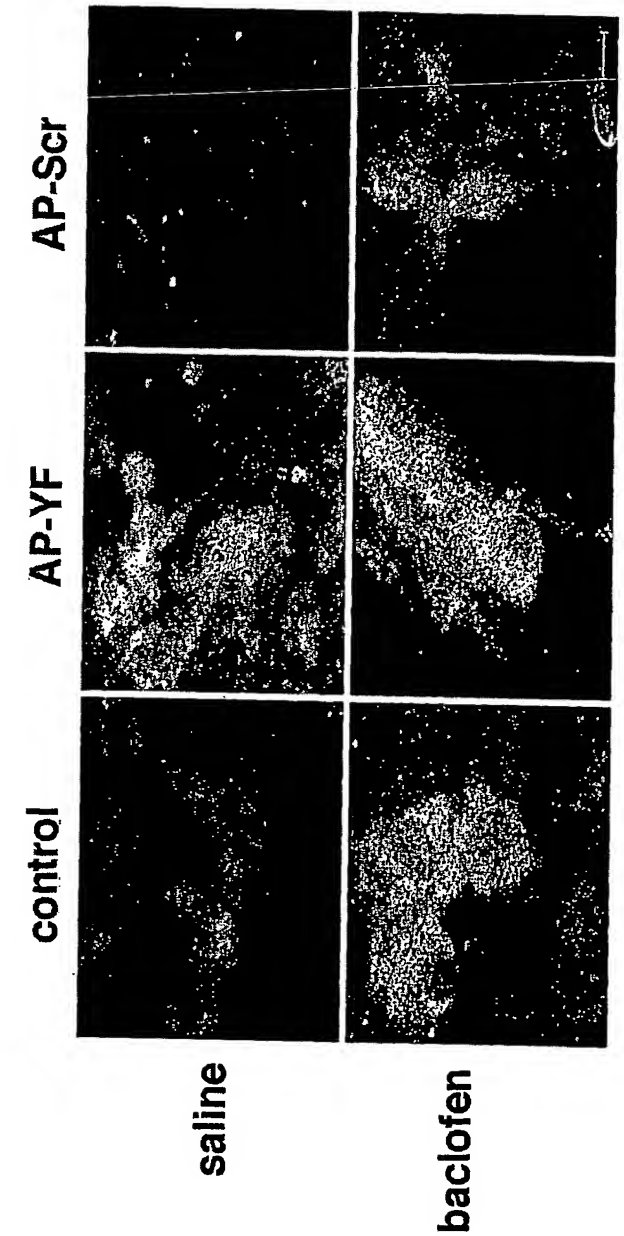


Figure 10

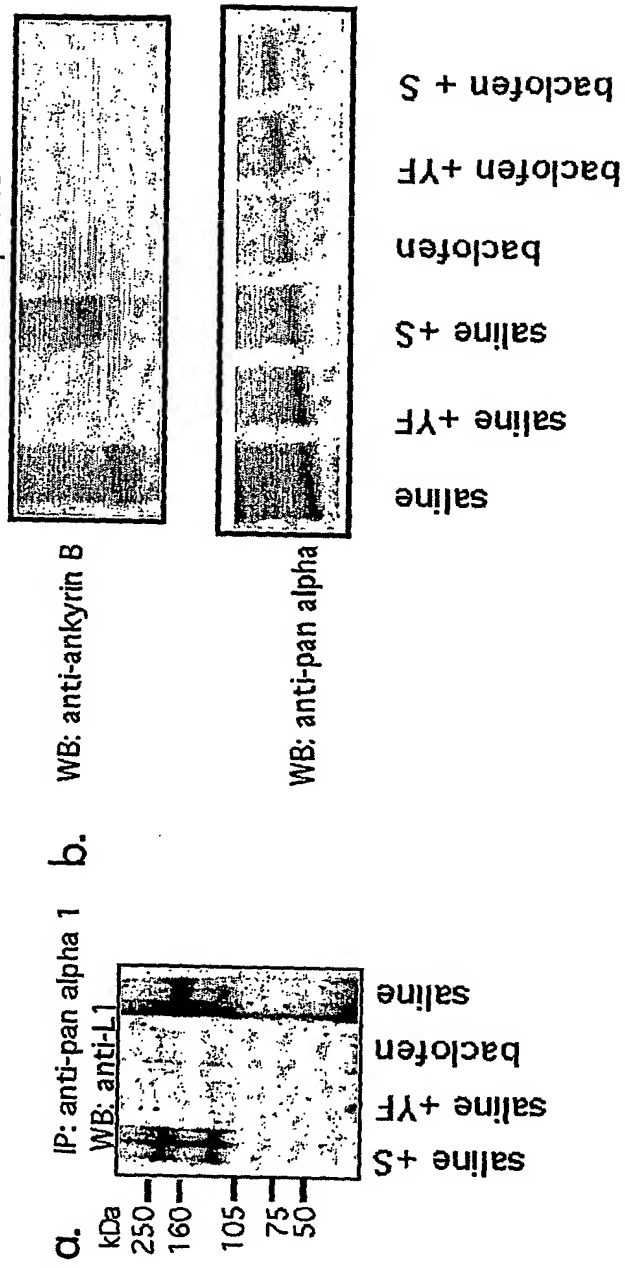

a.
IP: anti-pan alpha 1
WB: anti-L 1
kDa
250
160
105
75
50
saline +S
saline +YF
baclofen
saline
b.
IP: anti- alpha 1B
WB: anti-ankyrin B
WB: anti-pan alpha
saline
saline +YF
saline +S
baclofen
baclofen +YF
baclofen + S

Figure 11

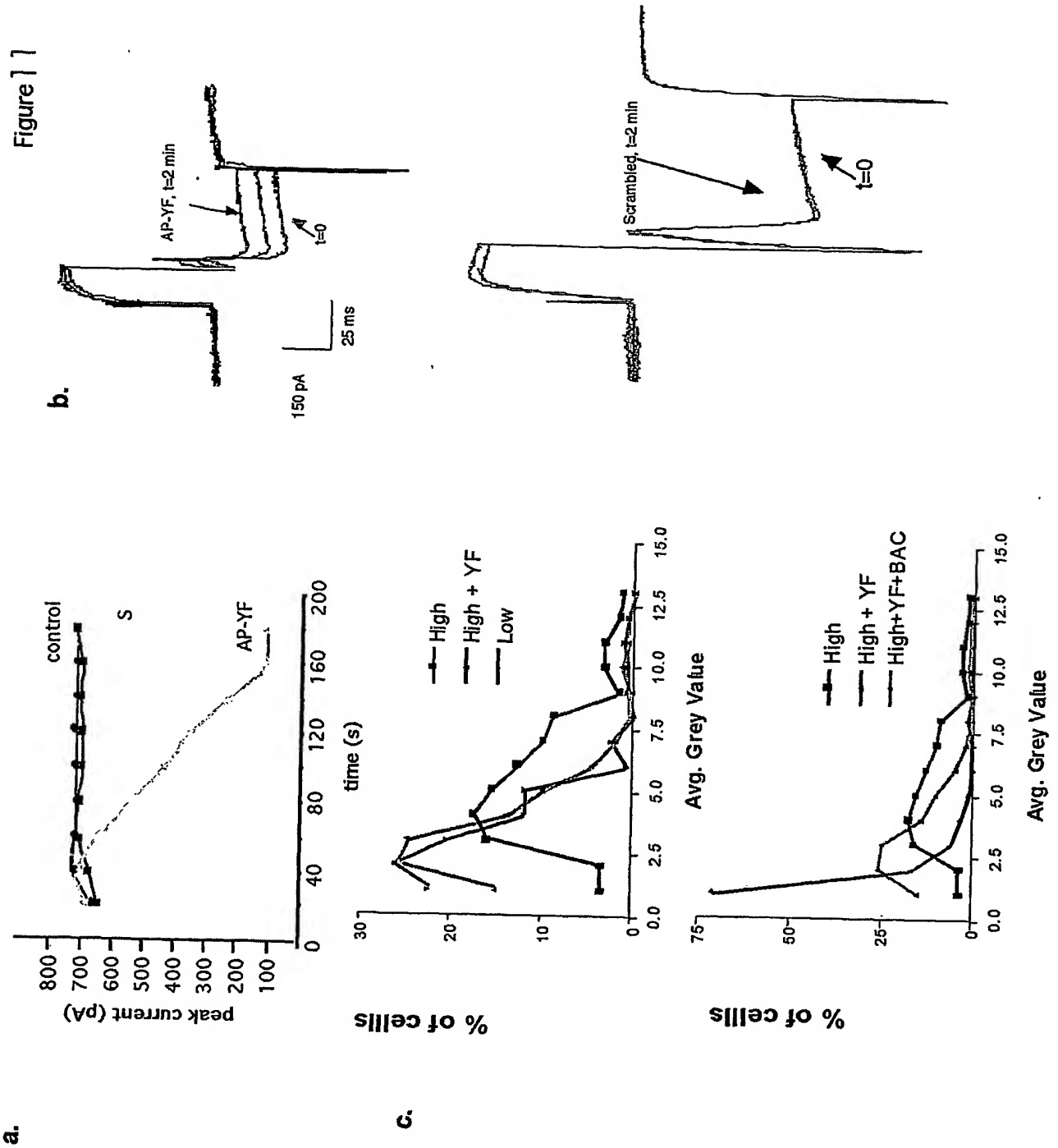
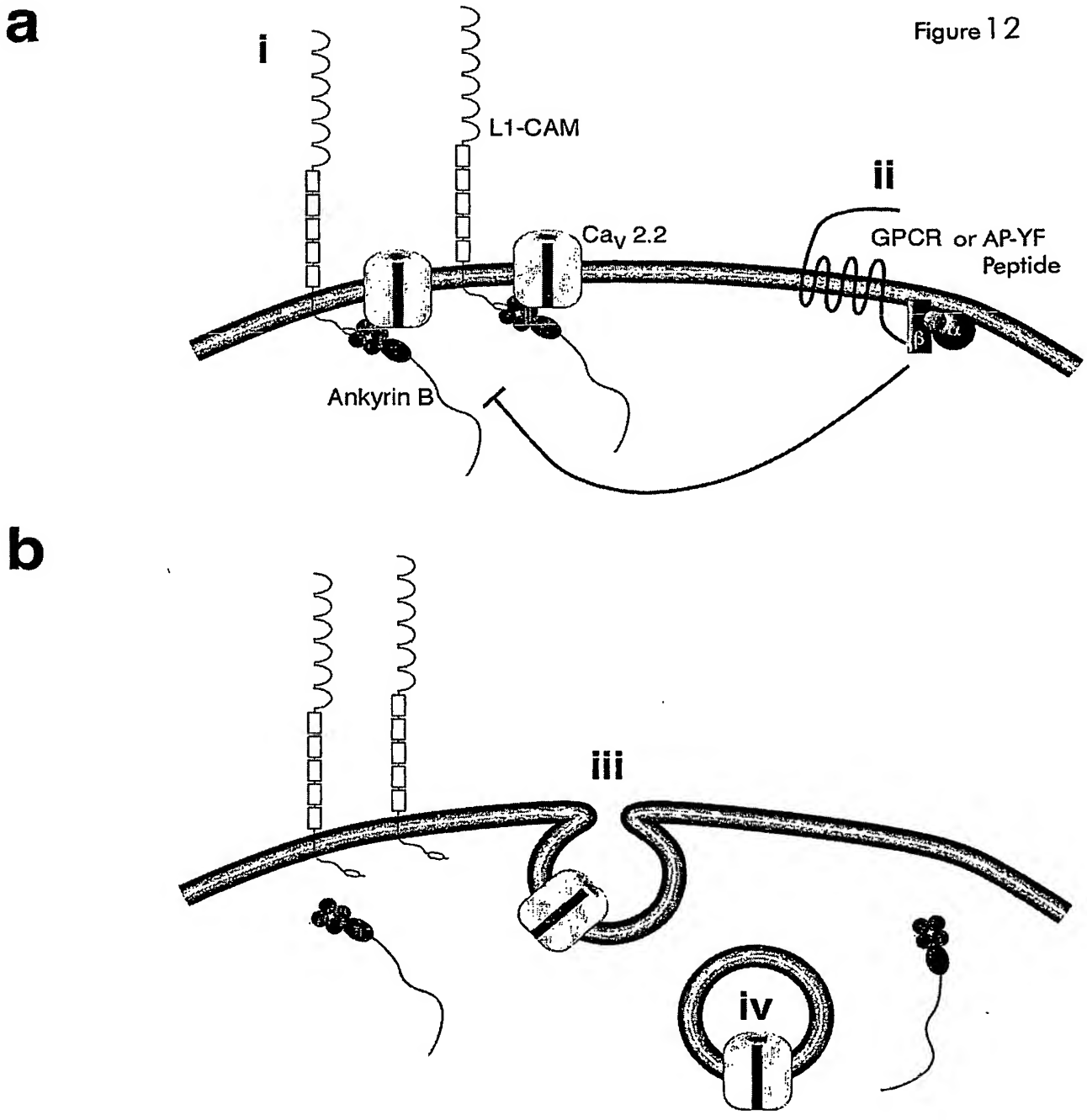

a.
control
S
AP-YF
peak current (pA)
800
700
600
500
400
300
200
100
0
40
80
120
160
200
time (s)
b.
AP-YF, t=2 min
t=0
150 pA
25 ms
Scrambled, t=2 min
t=0
c.
High
High + YF
Low
% of cells
Avg. Grey Value
High
High + YF
High+YF+BAC
% of cells
Avg. Grey Value

Figure 12



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